

09757992-042902

TCGACCCACGCGTCCGGGAGGATCGGGAGTCGCGGGAGGATGGGCCCGCGCTAGGCTCGCACTCCGGA
CGCGCCTCGC
AGTGGCGAGGGTGGGTGCCCCGCGCCTGCAGCGTCCGCCGGGGCGGCGCGGGGAGGTGGCCGACAG
GCTCCGGGCC
TCGCAGCCTCAGCCCCGGCCAGCGCGCTTTCCGACGGCGGCGCCGCGCCGAGCCACCCGCC
CGCCCAAGGTCTCTCGCGGGCGGGAGAACGGAACCTCCCAACTTCCTGAGTTCTAAAGTTCCTGTTG
CTTCAGACAA
TGGATGAGCAATCACAAGGAATGCAAGGGCCACCTGTTCCCTCAGTTCCAACCACAGAAGGCCCTTACGA
CCGGATATGG
GCTATAATACATTAGCCAACTTTTGAATAGAAAAGAAAATTGGTCGCGGACAATTTAGTGAAG
TTTATAGAGCAGCCTGTCTCTTGGATGGAGTACCAGTAGCTTTAAAAAAGTGCAGATATTTGATTTA
ATGGATGCCA
AAGCAGTGCTGATTGCATCAAAGAAATAGATCTTCTTAAGCAACTCAACCATCCAAATGTAATAAAA
TATTATGCAT
CATTCATTGAAGATAATGAACTAAACATAGTTTTGGAACTAGCAGATGCTGGCGACCTATCCA
GAATGATCAAGCATTTTAAGAAGCAAAAGAGGCTAATTCTTGAAAGAACTGTTTGAAGTATTTGTT
CAGCTTTGCA
GTGCATTGGAACACATGCATTCTCGAAGAGTCATGCATAGAGATATAAAACCAGCTAATGTGTTTCAAT
ACAGCCACTG
GGGTGGTAAACTTTGGAGATCTTGGGCTTGGCCGGTTTTTCAGCTCAAAAACCACAGCTGCAC
ATCTTTTAGTTGGTACGCCTTATTACATGTCTCCAGAGAGAAATACATGAAAATGGATACAACTTCAA
TCTGACATCT
GGTCTCTTGGCTGTCTACTATATGAGATGGCTGCATTACAAAGTCCTTTCTATGGTGACAAAATGAAT
TTATACTCAC
TGTGTAAGAAGATAGAACAGTGTGACTACCCACCTCTTCCTTCAGATCACTATTCAGAAGAAC
TCCGACAGTTAGTTAATATGTGCATCAACCCAGATCCAGAGAAGCGACCAGACGTCACCTATGTTTAT
GACGTAGCAA
AGAGGATGCATGCATGCACTGCAAGCAGCTAAACATGCAAGATCATGAAGAGTGAACCAAAGTAATT
GAAAGTATTT
TGTGCAAAGTCGTACCTSCCATTTATGTCTGGGTGTTAAGATTAATATTTTCAGAGCTAGTGT
GCTCTGAATCCTTAACCAGTTTTTCATATAAGCTTCATTTTGTACCAGTCACCTAAATCACCTCCTTGC
AACCCCAAA
TGACTTTGGAATAACTGAATTGCATGTTAGGAGAGAAAATGAAACATGATGGTTTTGAATGGCTAAAG
GTTTATAGAA
TTTCTTACAGTTTTTCTGCTGATAAATTGTGTTTAGATAGACTGTCAGTGCCAAATATTGAAGG
TGCAGCTTGGCACACATCAGAATAGACTCATACCTGAGAAAAAGTATCTGAACATGTGACTTGTCTCT
TTTTTAGTAA
TTTATGGACATTGAGATGAACACAATTGTGAACTTTTGTGAAGATTTTATTTTTAAACGTTTGAAGTA
CTAGTTTTAG
TTCTTAGCAGAGTAGTTTTCAAATATGATCTTATGATAAATGTAGACACAACTATTTGAGA
AACATTTAGAACTCTTAGCTTATACATTCAAAATGTAATTTAAATGTGAAGATTTGGGGACAAAAT
GTGAGTCAGA
CACTGAAGAGTTTTTTGTTTTGTTTTAATATTTTTGATATTCTCTTTCATTGAAATGGTATAAATGA
ATCCATTTAA
AAAGTGGTTAAGGATTTGTTTAGCTGGTGTGATAATAATTTTTAAAGTTGCACATTGCCCAAG
GCTTTTTTTGTGTGTTTTATTGTTGTTGTACATTTGAAAAATATTCTTTGAATAACCTTGCAGTAC
TATATTTCAA

Fig. 1

TTTCTTTTATAAATTTAAGTGCATTTTAACTCATAATTGTACACTATAATATAAGCCTAAGTTTTTTATT
 CATAAGTTTT
 ATTGAAGTTCTGATCGGTCCCCTTCAGAAATTTTTTTATATTATTCTTCAAGTTACTTTCTTA
 TTTATATTGTATGTGCATTTTATCCATTAATGTTTCATACTTTCTGAGAGTATAATACCCTTTTAAAA
 GATATTTGGT
 ATACCAATACTTTTCCTGGATTGAAAACCTTTTTTTAACTTTTTTAAAAATTTGGGCCACTCTGTATGCA
 TATGTTTGGT
 CTTGTTAAAGAGGAAGAAAGGATGTGTGTTTATACTGTACCTGTGAATGTTGATACAGTTACAA
 TTTATTTGACAAGGTTGTAATCTAGAATATGCTTAATAAAATGAAAACCTGGCCATGACTACAGCCAG
 AACTGTTATG
 AGATTAACATTTCTATTGAGAAGCTTTTGAGTAAAGTACTGTATTTGTTTCATGAAGATGACTGAGATG
 GTAACACTTC
 GTGTAGCTTAAGGAAATGGGCAGAAATTCGTAAATGCTGTTGTGCAGATGTGTTTTCCCTGAA
 TGCTTTCGTATTAGTGGCGACCAGTTTCTCACAGAATTGTGAAGCCTGAAGGCCAAGAGGAAGTCAC
 GTTAAAGGAC
 TCTGTGCCATCTTACAACCTTGGATGAATTATCCTGCCAACGTGAAAACCTCATGTTCAAAGAACACT
 TCCCTTTAGC
 CGATGTAAGTCTGGTTTTGTTTTTCATATGTGTTTTTCTTACACTCATTTGAATGCTTTCAA
 GCATTTGTAACTTAAAAAANWAWAAGGGCAAAAAGTCTGAACCTTGTTTTCTGAAATCTAATC
 AGTTATGTAT
 GGTTCCTGAAGGGTAATTTTATTTTGAATAGGTAAAGCGAAACCTGTTTTGTCWTGTTTTTCTGAG
 GGCTAGATGC
 ATTTTTTTTCTCACACTCTTAATGACTTTTAAACATTTTATACTGAGCATCCATAGATATATTC
 TAGAAGTATGAGAAGAATTATTCTTATTGACCATTAATGTCATGTTTCATTTTAAATGTAATATAATTGA
 GATGAAATGT
 TCTCTGGTTGGAACAGATACTCTCTTTTTTTTTTCTTGCAATCTTTAAGAATACATAGATCTAAAATTC
 ATTAGCTTGA
 CCCCTCAAAGTAACCTTTTAAAGTAAAGATTAAAGCTTTTCTTCTCAGTGAATATATCTGCTAGA
 AGGAAATAGCTGGGAAGAATTTAATGATCAGGGAAATTCATTATTTCTATATGTGGAACTTTTTGCT
 TCGAATATTG
 TATCTTTTTAAATCTAAATGTTTCATATTTTCTGGAAGAAACCACTGTGTAAAAATCAAATTTTAATT
 TTGAATGGAA
 TAATTTCAAAGAACTATGAAGATGATTTGAAGCTCTAATTTATATAGTCACCTATAAAATGTT
 CTTTATATGTGTTTCATAAGTAAATTTTATATTGATTAAAGTTAAACTTTTGAATTGATTTGAGGAGCAG
 TAAAAATGAAA
 GCTATATCTATTNCTAAACCYTATTTAGACATTGGKACCAGTTACCCAGGTGAAAATAKGGAGTAACT
 TTGTTTTGTA
 TGGTAAGGTTTAGGAATGGNGGATGAAGGGTATCTCTATATAAAATAAAGTGCTCAACAATGTG
 CAATGATTGTAAATTTAGTAAGATATTACAGCCATTTTCATGAATGCTTTACCATTCAACATAGTATCT
 ATTACAAAAC
 ACCTTTCTTGATCCATATACTTCAGGTGTTGCTGTTAACATTTACTATGATATTTATTTTAACCAA
 ATGTTACTCA
 CATTAATGTTTATTCTTTTAAATGAATGTATTATGTTTTTAACCCACAAATGCATACTTACC
 CTGTGCCTCATATTTCAATAGTACTGTAATATGGACATCTTTTGTGAAATACTTTTATTTTGTATGC
 TTTAAATATA
 CATAAAAAAGATTTCTGTTATTAGCTTTGAAAATGTATAATATCCTAATATAAACAAAAATATAAA
 AATAAAAAATG
 AATACAGTAAAAAAAAAAAAAAAAAAAAAAAAAGG

Fig. 1 (continued)

MDEQSQGMQGPVPQFQPKALRPDMGYNTLANFRIEKKIGRGQFSEVYRAACLLDGVVPVALKKVQIF
DLMDAKARAD
CIKEIDLLKQLNHPNVIKYYASFIEDNELNIVLELADAGDLSRMIKHFKKQKRLIPERTVWKYFVQLC
SALEHMHSRR
VMHRDIKPANVFITATGVVKLGDLGLGRFFSSKTTAAHSLVGTPPYMSPERIHENGYNFKSDI
WSLGCLLYEMAALQSPFYGDKMNLVSLCKIEQCDYPPLPSDHYSEELRQLVNMCIINPDPEKRPDVTY
VYDVAKRMHA
CTASS

Fig. 1 (continued)

206270-286450

00549-01000

GTCGACCCACGCGTCCGGTGGAAGTATAATACTTTGTCATTATGAGATGTCGTCTCTCGG
TGCTCTCTTTGTGCAAATTAATTTGATGACTTGCAGTTTTTTGAAAAGTGGGGTGGAGG
AAGTTTTGGGAGTGTTTATCGAGCCAAATGGATATCACAGGACAAGGAGGTGGCTGTAAA
GAAGCTCCTCAAAATAGAGAAAGAGGCAGAAATACTCAGTGTCTCAGTCACAGAAACAT
CATCCAGTTTTATGGAGTAATTCTTGAACCTCCCAACTATGGCATTGTACAGAAATATGC
TTCTCTGGGATCACTCTATGATTACATTAACAGTAACAGAAGTGAGGAGATGGATATGGA
TCACATTATGACCTGGGCCACTGATGTAGCCAAAGGAATGCATTATTTACATATGGAGGC
TCCTGTCAAGGTGATTCACAGAGACCTCAAGTCAAGAAACGTTGTTATAGCTGCTGATGG
AGTACTGAAGATCTGTGACTTTGGTGCCTCTCGGTCCATAACCATAACAACACACATGTC
CTTGGTTGGAACTTTCCCATGGATGGCTCCAGAAGTTATCCAGAGTCTCCCTGTGTGAGA
AACTTGTGACACATATTCCTATGGTGTGGTTCTCTGGGAGATGCTAACAAGGGAGGTCCC
CTTTAAAGGTTTGGAAAGGATTACAAGTAGCTTGGCTGTAGTGGAAGAAAACGAGAGATT
AACCATTCCAAGCAGTTGCCCCAGAAGTTTTGCTGAAGTGTACATCAGTGTGGGAAGC
TGATGCCAAGAAACGGCCATCATTCAAGCAAATCATTCAATCCTGGAGTCCATGTCAA
TGACACGAGCCTTCTGACAAGTGAACCTATTCTACACAACAAGCGGAGTGGAGGTG
CGAAATTGAGGCAACTCTTGAGAGGCTAAAGAACTAGAGCGTGATCTCAGCTTTAAGGA
GCAGGAGCTTAAAGAACGAGAAAGACGTTTAAAGATGTGGGAGCAAAGCTGACAGAGCA
GTCCAACACCCCGCTTCTCTTGCCTCTTGTGCAAGAATGTCTGAGGAGTCTTACTTTGA
ATCTAAAAACAGAGGAGTCAAACAGTGCAGAGATGTCATGTCAGATCACAGCAACAAGTAA
CGGGGAGGGCCATGGCATGAACCCAAGTCTGCAGGCCATGATGCTGATGGGCTTTGGGGA
TATCTTCTCAATGAACAAAGCAGGAGCTGTGATGCATTCTGGGATGCAGATAAACATGCA
AGCCAAGCAGAATTCTTCCAAAACCACATCTAAGAGAAGGGGGAAGAAAGTCAACATGGC
TCTGGGGTTCACTGATTTTTGACTTGTGCAAGGTGACGATGATGATGATGACGGTGA
GGAGGAGGATAATGACATGGATAATAGTGAATGAAAGCAGAAAGCAAAGTAATAAAATCA
CAAATGTTTGGAAAACACAAAAGTAACCTTGTATCTCAGTCTGTACAAAACAGTAAGG
AGGCAGAAAGCCAAGCACTGCATTTTTAGGCCAATCACATTTACATGACCGTAATTTCTT
ATCAATTCTACTTTTATTTTTTGCTTACAGAAAAACGGGGGGAGAATTAAGCCAAAGAAGT
ATATTTATGAATCAGCAAATGTGGTGCCTGATTATAGAAATTTGTGATCCTATATACAAT
ATAGGACTTTTAAAGTTGTGACATTCTGGCTTTTTCTTTTAAATGAATACTTTTTTAGTTTG
TATTTGACTTTATTTCTTTTATTCAAATCATTTTTTAAAACTTACATTTTGAACAAACAC
TCTTAACTCCTAATTGTTCTTTGACACGTAGTAATTCTGTGACATACTTTTTTTTTCTTA
TAGCAATACACTGTAATATCAGAAATGGTTGGCCTGAGCAACCTAGTAAGACCTCGTCTC
TACTAATAATTAAAAACTAGCTGGCATGGTAGCACACACCTGTAGTCCCAGATACTTGG
GAGGCCAAGGCAGGAGGATTGCTTGAGACCTAGCAATCAGTCAGGGCTGCAGTGAGCCAT
GATGGCACCACTGCACCTAGCCTGGGCAAGAGAACAAGATCCTGTCTCAAAAAACAAAA
AAAAAAAAAAGGGCGGCCG

MSSLGASFVQIKFDDLQFFENC GGGSFGSVYRAKWISQDKEVAVK
KLLKIEKEAEILSVLSHRNIIQFYGVILEPPNYGIVTEYASLGSPLYDYINSNRSEEMDM
HIMTWATDVAKGMHYLHMEAPVKVIHRDLKSRNVVIAADGVLKICDFGASRFHNHTHMS
LVGTFPWWAPEVIQSLPVSETCDTYSYGVVLWEMLTREVFPKGLEGLQVAWLVEKNERL
TIPSSCPRSFAELLHQWEADAKKRPSFKQIISILESMSNDTSLPDKCNSFLHNKAEWRC
EIEATLERLKKLERDLSFKEQELKERERRLKMWEQKLTEQSNTPLLLPLAARMSEESYFE
SKTEESNSAEMSCQITATSNGEHGMNPSLQAMMLMGFGDIFSMNKAGAVMHSGMQINMQ
AKQNSSKTTSKRRGKKVNMLGFSDFDLSEGDDDDDDGEEEDNDMDNSE

Fig. 2

CGGTGGTGGCGGCAGCGGCGGCTGCGGGGGACACGGGGCCGCGGCCACCATGGCCGTGC
GACAGGCGCTGGGCGCGGCCTGCAGCTGGGTGCGAGCGCTGCTGCTGCGCTTCACGGGGC
AGCCCCGCCGGGCCCTACGGCTTGGGGCGGCGGGCCCGGCGGGGCTGTGTCCGCGGGG
AGCGTCCAGGCTGGGCGCAGGACCGGGCGCGAGCCTCGCAGGGTTCGGGCTCGGGCTTC
CTAACCGTCTCCGCTTCTTCCGCCAGTGGTGGCCGGGCTGGCGGCGCGGTTCAGCGGC
AGTTCGTGGTGCGGGCCGGGGCTGCGCGGGCCCTTGGCGCCGGGCAGTCTTCTGGCCT
TCGGGCTAGGGCTGGGCTCATCGAGGAAAAACAGGCGGAGAGCCGGCGGGCGGTCTCGG
CCTGTGAGGAGATCCAGGCAATTTTACCCAGAAAAGCAAGCCGGGGCCTGACCCGTTGG
ACACGAGACGCTTGACGGGCTTTCGGCTGGAGGAGTATCTGATAGGGCAGTCCATTGGTA
AGGGCTGCAGTGCTGCTGTGTATGAAGCCACCATGCCCTACATTGCCCCAGAACCTGGAGG
TGACAAAGAGCACCGGGTTGCTTCCAGGGAGAGGCCCAGGTACCAGTGCACCAGGAGAAG
GGCAGGAGCGAGCTCCGGGGGGCCCCCTGCCTTCCCCCTTGGCCATCAAGATGATGTGGAACA
TCTCGGCAGGTTTCTCCAGCGAAGCCATCTTGAACACAATGAGCCAGGAGCTGGTCCCAG
CGAGCCGAGTGGCCTTGGCTGGGGAGTATGGAGCAGTCACTTACAGAAAATCCAAGAGAG
GTCCCAAGCAACTAGCCCCCTACCCCCAACATCATCCGGGTTCTCCGCGCCTTACCTCTT
CCGTGCCGCTGCTGCCAGGGGCCCTGGTGCAGTACCCTGATGTGCTGCCCTCACGCCTCC
ACCTTGAAGGCCTGGGCCATGGCCGGACGCTGTTCTCGTTATGAAGAACTATCCCTGTA
CCCTGCGCCAGTACCTTTGTGTGAACACACCCAGCCCCCGCCTCGCCGCCATGATGCTGC
TGCAGCTGCTGGAAGGCGTGGACCATCTGGTTCAACAGGGCATCGCGCACAGAGACCTGA
AATCCGACAACATCTTGTGGAGCTGGACCCAGACGGCTGCCCTGGCTGGTGTATCGCAG
ATTTTGGCTGCTGCCTGGCTGATGAGAGCATCGGCCTGCAGTTGCCCTTCAGCAGCTGGT
ACGTGGATCGGGGCGGAAACGGCTGTCTGATGGCCCCAGAGGTGTCCACGGCCCGTCTTG
GCCCCAGGGCAGTGATTGACTACAGCAAGGCTGATGCCCTGGGCAGTGGGAGCCATCGCCT
ATGAAATCTTCCGGCTTGTCAATCCCTTCTACGGCCAGGGCAAGGCCACCTTGAAAGCC
GCAGCTACCAAGAGGCTCAGCTACCTGCACTGCCCCAGTCACTGCCCTCCAGACGTGAGAC
AGTTGGTGAGGGCACTGCTCCAGCGAGAGGCCAGCAAGAGACCATCTGCCCGAGTAGCCG
CAATGTGCTTCATCTAAGCCTCTGGGGTGAACATATTCTAGCCCTGAAGAATCTGAAGT
TAGACAAGATGGTTGGCTGGCTCCTCCAACAATCGGCCGCCACTTTGTTGGCCAACAGGC
TCACAGAGAAGTGTGTGTGGAACAATAATGAAGATGCTCTTCTGGCTAACCTGGAGT
GTGAAACGCTCTGCCAGGCAGCCCTCCTCCTCTGCTCATGGAGGGCAGCCCTGTGATGTC
CCTGCATGGAGCTGGTGAATTACTAAAAGAACTTGGCATCCTCTGTGTGCTGATGGTCTG
TGAATGGTGAGGGTGGGAGTCAGGAGACAAGACAGCGCAGAGAGGGCTGGTTAGCCGGAA
AAGGCCCTCGGGCTTGGCAAATGGAAGAACTTGAGTGAGAGTTCAGTCTGCAGTCTCTGCT
TCACAGACATCTGAAAAGTGAATGGCCAAGCTGGTCTAGTAGATGAGGCTGGACTGAGGA
GGGGTAGGCCTGCATCCACAGAGAGGATCCAGGCCAAGGCACTGGCTGTGAGTGGCAGAG
TTTGGCTGTGACCTTTGCCCTTAACACGAGGAACTCGTTTGAAGGGGGCAGCGTAGCATG
TCTGATTTGCCACCTGGATGAAGGCAGACATCAACATGGGTGAGCAGCTTCACTTACGGG
AGTGGGAAATTACATGAGGCCTGGGCCCTTGCCTTCCCAAGCTGTGCGTTCTGGACCAGC
TACTGAATTATTAATCTCACTTAGCGAAAGTGACGGATGAGCAGTAAGTAAGTAAGTGTG
GGGATTTAACTTGAGGGTTTCCCTCCTGACTAGCCTCTCTTACAGGAATTGTGAAATAT
TAAATGCAAATTTACAACCTGCAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGGCC

Fig. 3

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Val	Arg	Gln	Ala	Leu	Gly	Arg	Gly	Leu	Gln	Leu	Gly	Arg	Ala	Leu	Leu	Met	Ala
		5					10						15				
Leu	Arg	Phe	Thr	Gly	Lys	Pro	Gly	Arg	Ala	Tyr	Gly	Leu	Gly	Arg	Pro		
	20					25					30						
Gly	Pro	Ala	Ala	Gly	Cys	Val	Arg	Gly	Glu	Arg	Pro	Gly	Trp	Ala	Ala		
	35				40					45					50		
Gly	Pro	Gly	Ala	Glu	Pro	Arg	Arg	Val	Gly	Leu	Gly	Leu	Pro	Asn	Arg		
				55					60						65		
Leu	Arg	Phe	Phe	Arg	Gln	Ser	Val	Ala	Gly	Leu	Ala	Ala	Arg	Leu	Gln		
			70					75						80			
Arg	Gln	Phe	Val	Val	Arg	Ala	Trp	Gly	Cys	Ala	Gly	Pro	Cys	Gly	Arg		
		85					90					95					
Ala	Val	Phe	Leu	Ala	Phe	Gly	Leu	Gly	Leu	Gly	Leu	Ile	Glu	Glu	Lys		
	100					105					110						
Gln	Ala	Glu	Ser	Arg	Arg	Ala	Val	Ser	Ala	Cys	Gln	Glu	Ile	Gln	Ala		
	115				120					125					130		
Ile	Phe	Thr	Gln	Lys	Ser	Lys	Pro	Gly	Pro	Asp	Pro	Leu	Asp	Thr	Arg		
				135					140					145			
Arg	Leu	Gln	Gly	Phe	Arg	Leu	Glu	Glu	Tyr	Leu	Ile	Gly	Gln	Ser	Ile		
			150					155					160				
Gly	Lys	Gly	Cys	Ser	Ala	Ala	Val	Tyr	Glu	Ala	Thr	Met	Pro	Thr	Leu		
		165					170					175					
Pro	Gln	Asn	Leu	Glu	Val	Thr	Lys	Ser	Thr	Gly	Leu	Leu	Pro	Gly	Arg		
	180					185					190						
Gly	Pro	Gly	Thr	Ser	Ala	Pro	Gly	Glu	Gly	Gln	Glu	Arg	Ala	Pro	Gly		
	195				200					205					210		
Ala	Pro	Ala	Phe	Pro	Leu	Ala	Ile	Lys	Met	Met	Trp	Asn	Ile	Ser	Ala		
				215					220					225			

Fig. 3 (continued)

005210-2864560

Gly	Ser	Ser	Ser	Glu	Ala	Ile	Leu	Asn	Thr	Met	Ser	Gln	Glu	Leu	Val	230	235	240
Pro	Ala	Ser	Arg	Val	Ala	Leu	Ala	Gly	Glu	Tyr	Gly	Ala	Val	Thr	Tyr	245	250	255
Arg	Lys	Ser	Lys	Arg	Gly	Pro	Lys	Gln	Leu	Ala	Pro	His	Pro	Asn	Ile	260	265	270
Ile	Arg	Val	Leu	Arg	Ala	Phe	Thr	Ser	Ser	Val	Pro	Leu	Leu	Pro	Gly	275	280	285
Ala	Leu	Val	Asp	Tyr	Pro	Asp	Val	Leu	Pro	Ser	Arg	Leu	His	Pro	Glu	295	300	305
Gly	Leu	Gly	His	Gly	Arg	Thr	Leu	Phe	Leu	Val	Met	Lys	Asn	Tyr	Pro	310	315	320
Cys	Thr	Leu	Arg	Gln	Tyr	Leu	Cys	Val	Asn	Thr	Pro	Ser	Pro	Arg	Leu	325	330	335
Ala	Ala	Met	Met	Leu	Leu	Gln	Leu	Leu	Glu	Gly	Val	Asp	His	Leu	Val	340	345	350
Gln	Gln	Gly	Ile	Ala	His	Arg	Asp	Leu	Lys	Ser	Asp	Asn	Ile	Leu	Val	355	360	365
Glu	Leu	Asp	Pro	Asp	Gly	Cys	Pro	Trp	Leu	Val	Ile	Ala	Asp	Phe	Gly	375	380	385
Cys	Cys	Leu	Ala	Asp	Glu	Ser	Ile	Gly	Leu	Gln	Leu	Pro	Phe	Ser	Ser	390	395	400
Trp	Tyr	Val	Asp	Arg	Gly	Gly	Asn	Gly	Cys	Leu	Met	Ala	Pro	Glu	Val	405	410	415
Ser	Thr	Ala	Arg	Pro	Gly	Pro	Arg	Ala	Val	Ile	Asp	Tyr	Ser	Lys	Ala	420	425	430

Fig. 3 (continued)

Asp Ala Trp Ala Val Gly Ala Ile Ala Tyr Glu Ile Phe Gly Leu Val
 435 440 445 450
 Asn Pro Phe Tyr Gly Gln Gly Lys Ala His Leu Glu Ser Arg Ser Tyr
 455 460 465
 Gln Glu Ala Gln Leu Pro Ala Leu Pro Glu Ser Val Pro Pro Asp Val
 470 475 480
 Arg Gln Leu Val Arg Ala Leu Leu Gln Arg Glu Ala Ser Lys Arg Pro
 485 490 495
 Ser Ala Arg Val Ala Ala Asn Val Leu His Leu Ser Leu Trp Gly Glu
 500 505 510
 His Ile Leu Ala Leu Lys Asn Leu Lys Leu Asp Lys Met Val Gly Trp
 515 520 525 530
 Leu Leu Gln Gln Ser Ala Ala Thr Leu Leu Ala Asn Arg Leu Thr Glu
 535 540 545
 Lys Cys Cys Val Glu Thr Lys Met Lys Met Leu Phe Leu Ala Asn Leu
 550 555 560
 Glu Cys Glu Thr Leu Cys Gln Ala Ala Leu Leu Leu Cys Ser Trp Arg
 565 570 575
 Ala Ala Leu

Fig. 3 (continued)

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T A L A K E L R E L R I E E T N R P M	19
G ACG GCA TTA GCC AAA GAA CTA AGA GAA CTC CGG ATT GAA GAA ACA AAC CGC CCA ATG	57
K K V T D Y S S S S E E S E S S E E E E	39
AAG AAG GTG ACT GAT TAC TCC TCC TCC AGT GAG GAG TCA GAA AGT AGC GAG GAA GAG GAG	117
E D G E S E T H D G T V A V S D I P R L	59
GAA GAT GGA GAG AGC GAG ACC CAT GAT GGG ACA GTG GCT GTC AGC GAC ATA CCC AGA CTG	177
I P T G A P G S N E Q Y N V G M V G T H	79
ATA CCA ACA GGA GCT CCA GGC AGC AAC GAG CAG TAC AAT GTG GGA ATG GTG GGG ACG CAT	237
G L E T S H A D S F S G S I S R E G T L	99
GGG CTG GAG ACC TCT CAT GCG GAC AGT TTC AGC GGC AGT ATT TCA AGA GAA GGA ACC TTG	297
M I R E T S G E K K R S G H S D S N G F	119
ATG ATT AGA GAG ACG TCT GGA GAG AAG AAG CGA TCT GGC CAC AGT GAC AGC AAT GGC TTT	357
A G H I N L P D L V Q Q S H S P A G T P	139
GCT GGC CAC ATC AAC CTC CCT GAC CTG GTG CAG CAG AGC CAT TCT CCA GCT GGA ACC CCG	417
T E G L G R V S T H S Q E M D S G T E Y	159
ACT GAG GGA CTG GGG CGC GTC TCA ACC CAT TCC CAG GAG ATG GAC TCT GGG ACT GAA TAT	477
G M G S S T K A S F T P F V D P R V Y Q	179
GGC ATG GGG AGC AGC ACC AAA GCC TCC TTC ACC CCC TTT GTG GAC CCC AGA GTA TAC CAG	537
T S P T D E D E E D E E S S A A A L F T	199
ACG TCT CCC ACT GAT GAA GAT GAA GAG GAT GAG GAA TCA TCA GCC GCA GCT CTG TTT ACT	597
S E L L R Q E Q A K L N E A R K I S V V	219
AGC GAA CTT CTT AGG CAA GAA CAG GCC AAA CTC AAT GAA GCA AGA AAG ATT TCG GTG GTA	657
N V N P T N I R P H S D T P E I R K Y K	239
AAT GTA AAC CCA ACC AAC ATT CGG CCT CAT AGC GAC ACA CCA GAA ATC AGA AAA TAC AAG	717
K R F N S E I L C A A L W G V N L L V G	259
AAA CGA TTC AAC TCA GAA ATA CTT TGT GCA GCT CTG TGG GGT GTA AAC CTT CTG GTG GGG	777
T E N G L M L L D R S G Q G K V Y N L I	279
ACT GAA AAT GGC CTG ATG CTT TTG GAC CGA AGT GGG CAA GGC AAA GTC TAT AAT CTG ATC	837
N R R R F Q Q M D V L E G L N V L V T I	299
AAC CGG AGG GGA TTT CAG CAG ATG GAT GTG CTA GAG GGA CTG AAT GTC CTT GTG ACA ATT	897
S G K K N K L R V Y Y L S W L R N R I L	319
TCA GGA AAG AAG AAT AAG CTA CGA GTT TAC TAT CTT TCA TGG TTA AGA AAC AGA ATA CTA	957
H N D P E V E K K Q G W I T V G D L E G	339
CAT AAT GAC CCA GAA GTA GAA AAG AAA CAA GGC TGG ATC ACT GTT GGG GAC TTG GAA GGC	1017

Fig. 5

C I H Y K V V K Y E R I K F L V I A L K 359
 TGT ATA CAT TAT AAA GTT GTT AAA TAT GAA AGG ATC AAA TTT TTG GTG ATT GCC TTA AAG 1077

 N A V E I Y A W A P K P Y H K F M A F K 379
 AAT GCT GTG GAA ATA TAT GCT TGG GCT CCT AAA CCG TAT CAT AAA TTC ATG GCA TTT AAG 1137

 S F A D L Q H K P L L V D L T V E E G Q 399
 TCT TTT GCA GAT CTC CAG CAC AAG CCT CTG CTA GTT GAT CTC ACG GTA GAA GAA GGT CAA 1197

 R L K V I F G S H T G F H V I D V D S G 419
 AGA TTA AAG GTT ATT TTT GGT TCA CAC ACT GGT TTC CAT GTA ATT GAT GTT GAT TCA GGA 1257

 N S Y D I Y I P S H I Q G N I T P H A I 439
 AAC TCT TAT GAT ATC TAC ATA CCA TCT CAT ATT CAG GGC AAT ATC ACT CCT CAT GCT ATT 1317

 V I L P K 444
 GTC ATC TTG CCT AAA 1332

Fig. 5 (continued)

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